



Konrad BASLER et al
USSN 10/664,859-Q77377
REPLACEMENT SHEET

FIGURE 1A



wild type

sev-wg

sev-wg, $lgs^{S17}/+$

FIGURE 1B



FIGURE 1C

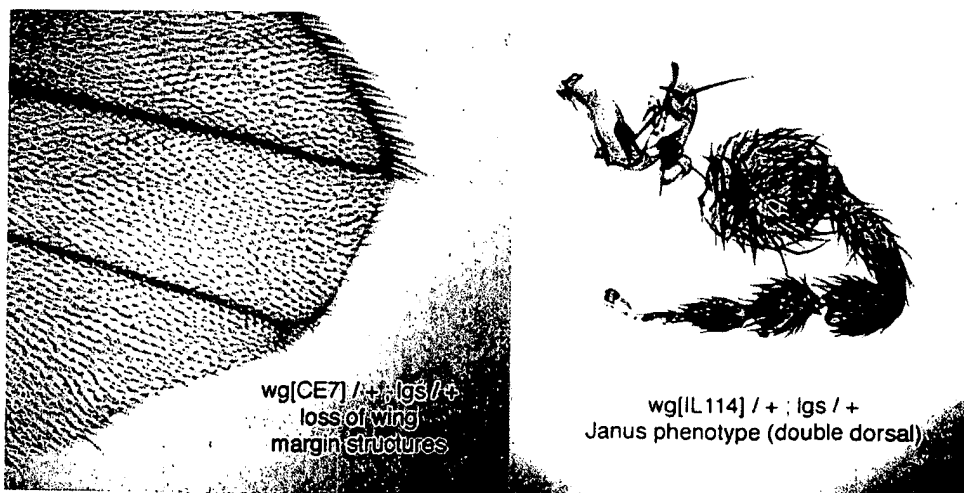


FIGURE 1A



wild type

sev-wg

sev-wg, lgs^{S17}/+

FIGURE 1B



FIGURE 1C

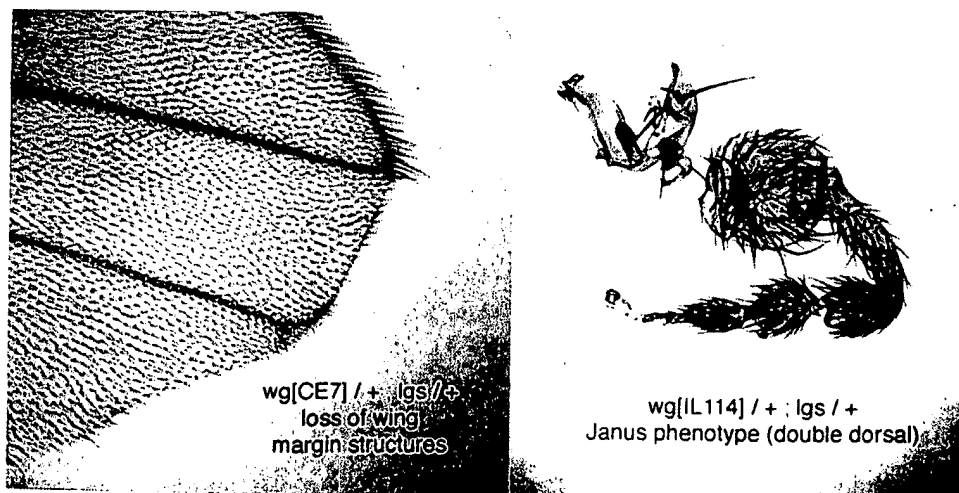


FIGURE 1A

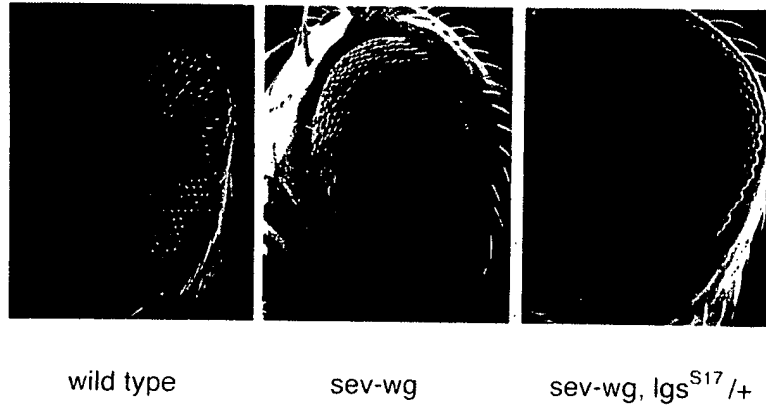


FIGURE 1B



FIGURE 1C

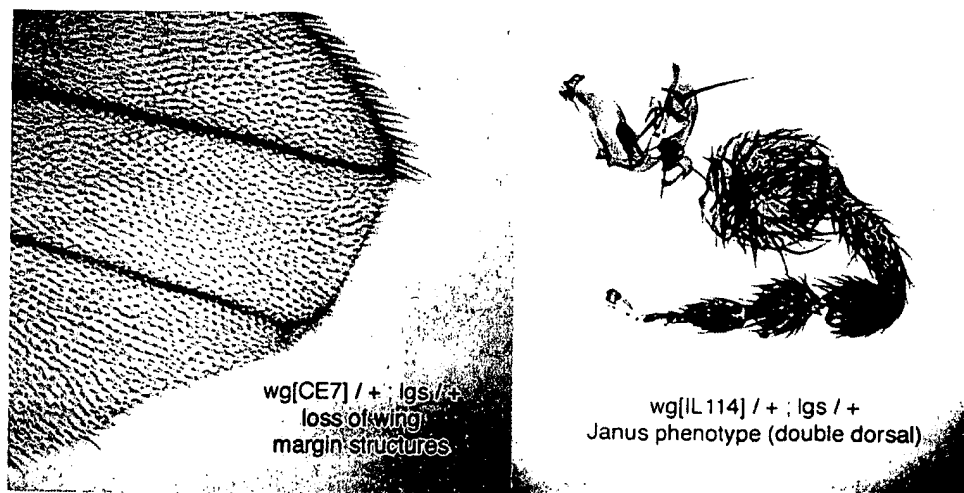


FIG. 2A

ACGAGTGCCTCTCTTATTATGCGAGCTGTTTATTCCAAAGTATGTTTCGCAATTTTCGACT 60
CCTGCTAACATAACGCACGGTTAAAGCAGGAACATTTGGGCCTATAAGCCCAAATTTCA 120
TTAGCTTAATACGATGCTCCGAAGTGTATTGTCATTTGCACATATACATAAAATTGTGAC 180
ATAGAATAGGAGAATTCCACATACAAATACAAAATACAAAATCCTCCAGTAAAATTTAA 240
AACGATATCGTGTGTTTTCGCTTCGCGTATCTCACGTGAGATGTAATCGCATGCATATGAGTG 300
GTGAGTGCCTGCGTGCAGTTCTTGGTCTAAATATGCTTAATTGCGTTCGCGGACTTCAAA 360
AGCAATAAAACGATGGATTTTAAATGCTACTTGAGCAATTAGCCACACAAGGGATCTTGG 420
GAAGGTCGATTTGAAGGAATTCGATTTCTAGGATGCTCTCGACAACAATGCCCCGAGTC 480
M P R S P 5
CAACCCAACAACAGCCGCAACCAAACTCCGATGCCTCCTCAACAAGTGCATCTGGATCAA 540
T Q Q Q P Q P N S D A S S T S A S G S N 25
ATCCTGGAGCAGCGATCGGAAATGGGGACTCGGCGGCGAGCAGAAGTTCTCCGAAGACCC 600
P G A A I G N G D S A A S R S S P K T L 45
TTAATAGCGAACCCTTTTCTACTTTGTGCGCGGGTAAGACTTGTATTGATTTCTCTTTGT 660
N S E P F S T L S P 55
CCGGAATTATAACAACCTTTCTGTGTTTCCAGATCAAATAAAATTGACGCCAGAAGAAGGC 720
D Q I K L T P E E G 65
ACTGAGAAAAGCGGACTATCAACTAGTGATAAAGCTGCCACTGGAGGAGCCCCAGGCAGT 780
T E K S G L S T S D K A A T G G A P G S 85
GGAAATAATCTGCCCAGGGACAACTATGCTAAGGCAGAAGTCTACGAGCACAATCAAC 840
G N N L P E G Q T M L R Q N S T S T I N 105
TCGTGCCTAGTCGCTTCTCCACAAACTCCAGTGAACACTCGAATAGCAGCAATGTGTCT 900
S C L V A S P Q N S S E H S N S S N V S 125
GCTACAGTGGGCCTTACTCAGATGGTAGATTGTGACGAGCAATCGAAGAAAAACAAATGT 960
A T V G L T Q M V D C D E Q S K K N K C 145
AGTGTGAAGGACGAGGAAGCTGGTAAGACTGCCCTACAAATGGTTTAAATTTTAAATG 1020
S V K D E E A 152
TATTGGCGTTCACCTTTGTTAATCATTTAATTGTTTTTTTTTTGCTATACTTACAATTTT 1080
AGTTTTAAACTTGTAACCTTGACTAAAACCTCGCGAAGCTCGGATCAAAACAGACATTTTC 1140
TTGGAACCGTAATTAAGCTCATAAAATATTAATTCATCTTGATGGAATGCATATCATAG 1200

FIG. 2B

<u>ATG TACTCAAACATCTCAAGAAAGACCTCAAATTGGATCAACTAATTAGTTTGAGAAAAA</u>	1260
<u>ATTGCTGTACTTTTAAGAATATATTAATTTAAAAATTTGCTGAGTGAAATGATATAATAG</u>	1320
<u>TCACAATAATTTTAGTTAAACTGCTAAAGCATTTTGAATAGCCGTGCTACGCAGATGCT</u>	1380
<u>ACTAGACGCGGTGTAAAAGCTAATTTTTATTTAAAGCTGTCCTAATATTCCATAACCAT</u>	1440
<u>TAATGTCCCATTTTCAGAAATAAGTTCTAATAAAGCAAAGGTCAAGCAGCTGGTGCGGC</u>	1500
E I S S N K A K G Q A A G G G	167
<u>TGCGAAACAGGTTCTACATCCAGTTTGACTGTCAAGGAAGAACCCACCGATGTCTTAGGC</u>	1560
C E T G S T S S L T V K E E P T D V L G	187
<u>AGTTTAGTAAATATGAAAAAGAAGAAAGAGAAAAATCATTGCGCAACGATGTCCCCTGTT</u>	1620
S L V N M K K E E R E N H S P T M S P V	207
<u>GGTTTTGGTTCAATTGGTAATGCACAGGACAACCTCGCTACACCGGTAAGTTTAAAGAG</u>	1680
G F G S I G N A Q D N S A T P	222
<u>ATCCATATAAAGCAAATAACAAGAATTAATGTCAGTTACCAATTTTATTTGATAGTCAA</u>	1740
<u>GAACTACTATAGCGATATCTCCTGCCTTTTAATTTTATTTTAATTAGGAAATACGAATAT</u>	1800
<u>TTCTAATTGTAAAATAAAATTGATTAATTAAGTAGAATTAAAAACCTTTTGAATTAGG</u>	1860
<u>ACATACCCCTTCCAAAAATCAGTAATCATTGGGAACGAGAGTGTGGTCCCGAAGGAGACTA</u>	1920
<u>CTATAAAACCTTTTGAGCTATCTGATACTGCACGCTACTAAAAATGATTAGTTTAGGAA</u>	1980
<u>ATGGGTGTAATTTGTAGGAAGTTTTCATTTTAGAAGAAATGTGATTATTTTATTAAACC</u>	2040
<u>CCTTCAAGCGGAACCTACATTTGTTCTACGATATTTTGGAAAAACAAATGGTTAAGTTGGA</u>	2100
<u>AAGTGCCTATAAAACAGAATTCCACGGTTTCAAATACTAACCAGGTTTTTGATTTAATTT</u>	2160
<u>TGATTAAATGAGAAATTATCACACTTCAGTTAAATGTTTAATTCGATTAAGGTCGGACA</u>	2220
<u>ATCACAGCAGATTCCATTTTTCGCTGTATATATAGAAGTCGCCTTCACACTCTTCTGGC</u>	2280
<u>GCGCTTCACCACTACGTGGAGTTCCGCCCGCAGTGATTTATATAGATGATTTACGAGTTA</u>	2340
<u>TTAATTTTTTTATGGTGTATTTTAATAAATATCTTATTTATTCATTTTACATAGTTAAAA</u>	2400
V K I	225
<u>TTGAAAGAATTTCAAACGACAGTACCACGGAAAAAAAGGATCGTCCTTGACAATGAATA</u>	2460
E R I S N D S T T E K K G S S L T M N N	245
<u>ATGACGAAATGAGCATGGAAGGCTGCAATCAGTTGAATCCCGATTTTATCAATGAATCTT</u>	2520
D E M S M E G C N Q L N P D F I N E S L	265

FIG. 2C

TAAATAATCCTGCAATTCGAGCATATTAGTAAGCGGAGTAGGACCAATACCCGGAATCG	2580
N N P A I S S I L V S G V G P I P G I G	285
GAGTTGGAGCGGGGACGGGAAATTTATTGACTGCCAACGCCAATGGAATCTCCTCGGGTA	2640
V G A G T G N L L T A N A N G I S S G S	305
GCAGTAATTGTTTGGATTACATGCAACAGCAAAATCACATATTCGTGTTTCAACTCAGC	2700
S N C L D Y M Q Q Q N H I F V F S T Q L	325
TGGCCAACAAAGGGGCCGAATCAGTTTTAAGCGGTCAATTTCAAACATATTATGCGTATC	2760
A N K G A E S V L S G Q F Q T I I A Y H	345
ACTGCACTCAGCCTGCTACAAAAAGCTTCTCGGAAGACTTTTTATGAAAAACCTTTAA	2820
C T Q P A T K S F L E D F F M K N P L K	365
AGATTAACAAGTTACAGCGGCACAATTCGTCGGTATGCCATGGATAGGCATGGGGCAGG	2880
I N K L Q R H N S V G M P W I G M G Q V	385
TTGGACTAACTCCTCCTAATCCTGTAGCCAAAATAACACAACAGCAGCCACATACAAAGA	2940
G L T P P N P V A K I T Q Q Q P H T K T	405
CCGTAGGCCTATTGAAACCCCAATTCAATCAACATGAAAACAGCAAACGTAGTACTGTAA	3000
V G L L K P Q F N Q H E N S K R S T V S	425
CGCGCCTAGCAACTCTTTTGTGACCACTCTGATCCTATGGGCAACGAAACTGAATTGA	3060
A P S N S F V D Q S D P M G N E T E L M	445
TGTGCTGGGAAGGCGGATCCTCAAACACCAGTAGGTCTGGACAAAACCTCACGAAATCATG	3120
C W E G G S S N T S R S G Q N S R N H V	465
TAGACAGTATCAGTACATCCAGCGAGTCACAGGCAATAAAGATACTGGAAGCAGCTGGCG	3180
D S I S T S S E S Q A I K I L E A A G V	485
TTGATTTGGGACAGGTCACAAAAGGAAGCGATCCTGGCCTGACAACTGAAAACAACATTG	3240
D L G Q V T K G S D P G L T T E N N I V	505
TATCACTGCAAGGAGTTAAGGTTCCAGACGAAAACCTTACACCACAACAGCGGCAACATC	3300
S L Q G V K V P D E N L T P Q Q R Q H R	525
GGGAAGAACAGTTGGCAAAAATAAAAAAATGAATCAATTTCTTTTCTGAAAATGAGA	3360
E E Q L A K I K K M N Q F L F P E N E N	545
ATTCACTAGGAGCTAATGTAAGCTCACAGATAACAAAAATTCAGGAGATTTAATGATGG	3420
S V G A N V S S Q I T K I P G D L M M G	565
GGATGTCGGGTGGCGGAGGCGGATCTATTATAAATCCGACGATGCGACAACCTGCATATGC	3480
M S G G G G S I I N P T M R Q L H M P	585
CAGGTAACGCCAATCGGAGCTCTATCGGCGACAAGTTCAGGACTTTCGGAAGATGTAA	3540
G N A K S E L L S A T S S G L S E D V M	605

FIG. 2D

TGCATCCAGGGGATGTTATATCAGATATGGGTGCCGTAATAGGATGTAATAATAATCAAA 3600
H P G D V I S D M G A V I G C N N N Q K 625

AAACCAGTGTGCAATGTGGATCTGGAGTAGGTGTTGTCACCTGGAACAACCTGCAGCTGGAG 3660
T S V Q C G S G V G V V T G T T A A G V 645

TAAATGTCAATATGCATTGCTCAAGCTCCGGCGCCCCGAATGGCAATATGATGGGAAGCT 3720
N V N M H C S S S G A P N G N M M G S S 665

CTACGGATATGCTAGCCTCGTTTGGCAACACAAGCTGCAACGTCATCGGAACGGCCCCAG 3780
T D M L A S F G N T S C N V I G T A P D 685

ATATGTCTAAGGAAGTTTAAATCAAGATAGCCGAACCCATTACATCAAGGGGGAGTTG 3840
M S K E V L N Q D S R T H S H Q G G V A 705

CTCAAATGGAGTGGTCGAAGATTCAACATCAATTTTTCGAAGAACGCCTCAAGGGGGGCA 3900
Q M E W S K I Q H Q F F E E R L K G G K 725

AGCCCAGACAAGTCACTGGAACCTGTAGTACCACAACAGCAAACCCCTTCTGGATCTGGTG 3960
P R Q V T G T V V P Q Q Q T P S G S G G 745

GAAACTCGTTAAACAACCAGGTGCGACCCCTGCAAGGTCCACCTCCTCCTTACCACTCCA 4020
N S L N N Q V R P L Q G P P P P Y H S I 765

TCCAGAGATCTGCGTCAGTACCAATAGCCACTCAATCGCCCAATCCCTCGAGTCCAAACA 4080
Q R S A S V P I A T Q S P N P S S P N N 785

ATCTATCTCTCCCGTCACCGCGGACAACCGCAGCAGTCATGGGATTGCCGACCAACTCTC 4140
L S L P S P R T T A A V M G L P T N S P 805

CTAGCATGGATGGAACAGGATCATTATCTGGATCTGTTCCGCAAGCTAATACTTCGACGG 4200
S M D G T G S L S G S V P Q A N T S T V 825

TTCAGGCAGGCACAACAACAGTGCTCTCAGCAAACAAGAACTGTTTTTCAGGCAGACACCC 4260
Q A G T T T V L S A N K N C F Q A D T P 845

CATCGCCGTCAAATCAAAATCGTAGTAGAAATACCGGATCGTCAAGCGTTCTTACGCATA 4320
S P S N Q N R S R N T G S S S V L T H N 865

ACTTAAGCAGCAACCCAAGTACCCCTTATCTCATCTATCCCCAAAGGAATTTGAGTCTT 4380
L S S N P S T P L S H L S P K E F E S F 885

TCGGTCAGTCCTCTGCTGGTATGTTATATTTGTTTAATTTTTTTAAAGACAAATCAAATA 4440
G Q S S A 890

TGAATTGCGTTAATAATAAGTTATATATTACATAACTCGGAAATTTGATAGAAAAAATCA 4500

GGAATAGAAAAATAAATTATTTTCCGGACCGCCCATCCATTCTTGAATCCAATTTCTG 4560

GAGTGATTGTTAGAGATAATCTACTATTAAAATTAAACACGAAAATTCATATCCGTTAAT 4620

FIG. 2E

<u>TGAAAATCACTATTGTTTAATAAGAAATTAAAAATATGTTTATTATAATATTTCTACAGG</u>	4680
G	891
TGATAACATGAAAAGTAGGCGACCAAGCCCACAGGGTCAGCGGTCACCAGTAAATAGTCT	4740
D N M K S R R P S P Q G Q R S P V N S L	911
AATAGAGGCAAATAAAGATGTACGATTGCTGCATCCAGTCCTGGTTTTAACCCGCATCC	4800
I E A N K D V R F A A S S P G F N P H P	931
ACATATGCAAAGCAATTCAAATTCAGCATTAAACGCCTATAAAATGGGCTCTACCAATAT	4860
H M Q S N S N S A L N A Y K M G S T N I	951
ACAGATGGAGGTAAATATTTAAATATTTTATTTAACGTTTTTGTGTTAATTTATCTTCTT	4920
Q M E	954
<u>TTTCAGCGTCAAGCATCAGCGCAAGGTGGATCCGTACAATTTAGTCGGCGCTCCGATAAT</u>	4980
R Q A S A Q G G S V Q F S R R S D N	972
ATTCCGCTAAATCCCAATAGTGGCAATCGGCCGCCACCAAACAAGATGACCCAAAACCTC	5040
I P L N P N S G N R P P P N K M T Q N F	992
GATCCAATCTCTTCTTTGGCACAAATGTCCCAACAATAACAAGTTGCGTGTCCAGCATG	5100
D P I S S L A Q M S Q Q L T S C V S S M	1012
GGTAGTCCAGCCGGAAGTGGTGGTATGACGATGATGGGGGGTCCGGGACCGTCCGACATC	5160

FIG. 2F

legless

G S P A G T G G M T M M G G P G P S D I	1032
AATATTGAGCATGGAATAATTTCTGGGACTAGATGGATCAGGAATAGATACCATAAATCAA	5220
N I E H G I I S G L D G S G I D T I N Q	1052
AATAACTGTCATTCAATGAATGTCGTAATGAACTCAATGGGTCCCCGAATGCTGAATCCT	5280
N N C H S M N V V M N S M G P R M L N P	1072
AAAATGTGCGTAGCAGGCGGTCCAAATGGACCGCTGGCTTTAATCCTAATTTCCCCCAAT	5340
K M C V A G G P N G P P G F N P N S P N	1092
GGTGGATTAAGAGAGAATTCCATAGGGTCTGGCTGTGGCTCAGCAAACCTCTTCAAACCTT	5400
G G L R E N S I G S G C G S A N S S N F	1112
CAAGGGGTTGTTCCACCTGGTGCCAGAATGATGGGTGCAATGCCAGTCAATTTTGGTTG	5460
Q G V V P P G A R M M G R M P V N F G S	1132
AATTCAATCCGAATATTTCAGGTAAAGGCGAGTACCCCAAACACCATAACAATACATGCCA	5520
N F N P N I Q V K A S T P N T I Q Y M P	1152
GTAAGGGCACAGAACGCCAACAACAATAACAACAATGGAGCTAATAATGTGCGAATGCCA	5580
V R A Q N A N N N N N N G A N N V R M P	1172
CCTAGTCTGGAATTTTTGTCAGAGGTACGCTAACCCCTCAAATGGGTGCTGTAGGCAATGGG	5640
P S L E F L Q R Y A N P Q M G A V G N G	1192
TCGCCAATATGCCACCATCAGCCAGCGACGGTACTCCTGGAATGCCAGGATTGATGGCG	5700
S P I C P P S A S D G T P G M P G L M A	1212
GGACCAGGAGCCGGAGGTATGCTAATGAATTCTTCCGGAGAGCAACACCAGAACAAGATC	5760
G P G A G G M L M N S S G E Q H Q N K I	1232
ACAAACAATCCTGGGGCAAGCAATGGTATTAATCTTCTTTCAGAATTGCAATCAAATGTCT	5820
T N N P G A S N G I N F F Q N C N Q M S	1252
ATTGTTGACGAAGAGGGTGGATTACCCGGCCATGACGGATCAATGAATATTGGTCAACCA	5880
I V D E E G G L P G H D G S M N I G Q P	1272
TCTATGATAAGGGGCATGCGTCCACATGCCATGCGGCCAAATGTAATGGGTGCGCGGATG	5940
S M I R G M R P H A M R P N V M G A R M	1292
CCACCCGTTAACAGGCAAATTCAGTTTGACAGTCATCGGATGGTATTGACTGTGTCTGGG	6000
P P V N R Q I Q F A Q S S D G I D C V G	1312
GATCCGTCATCATTTTCTACTAACGCTTCTGCAACAGCGCTGGACCACACATGTTTGA	6060
D P S S F F T N A S C N S A G P H M F G	1332
TCAGCACAACAGGCCAATCAGCCTAAGACACAACACATAAAGAACATACCTAGTGAATG	6120
S A Q Q A N Q P K T Q H I K N I P S G M	1352

FIG. 2G

TGTCAAAACCAATCGGGACTTGCAAGTGGCACAAGGGCAGATCCAAGTGCATGGGCAAGGA	6180
C Q N Q S G L A V A Q G Q I Q L H G Q G	1372
CATGCGCAGGGTCAGTCTTTAATTGGACCTACTAATAATAATTTAATGTCAACTGCCGGA	6240
H A Q G Q S L I G P T N N N L M S T A G	1392
AGTGTCAAGTGTACTAACGGTGTCTCTGGCATCAATTTTCGTAGGTCCCTCTTCTACGGAC	6300
S V S A T N G V S G I N F V G P S S T D	1412
CTGAAGTATGCCCAGCAATATCATAGTTTTTCAGCAGCAGTTATATGCTACCAACACCAGA	6360
L K Y A Q Q Y H S F Q Q Q L Y A T N T R	1432
AGTCAACAACAACAGCATATGCACCAGCAGCACCAGAGCAACATGATAACAATGCCGCCG	6420
S Q Q Q Q H M H Q Q H Q S N M I T M P P	1452
AATTTATCACCAATCCAACGTTCTTTGTCAACAAATAAACTTCTAAATTTTGGCCGCC	6480
N L S P N P T F F V N K *	1465
TCGTCATGTATTGTTTACTAGTCTCCAAATTAAGACATGCATCTCTAAATAAGATTTTTT	6540
GAAGCTTATTTACTTAGGTGTTTTTACAACGGAGAAAAATAAACTTTTGGATATGCAAATG	6600
ATAACGTTGGAACAACATAATTCATTTGCAACTTTTAGAAGTCACGTCGAAGTTAAATG	6660
TAGAATCTGTATTTTAACATAATAGGTCACTGTAAAAATAATTAACATCGAAATTTTA	6720
GTTATCAGCAGCTATTTTCTGTTATTATTTAATATGTGCGCTGCTCTCTGTGTAAAT	6780
GAAATTAAATATATATATAAATGTAAAACGCTATTGATATATATTGCTCTCAACTGTAT	6840
TGTAATCAATATTAAGAGAACTGTAAATCTTCCATATAAAGGTAATGAAAAAAAAAAAA	6900
AAAAAAAAA	6909

FIG. 3A

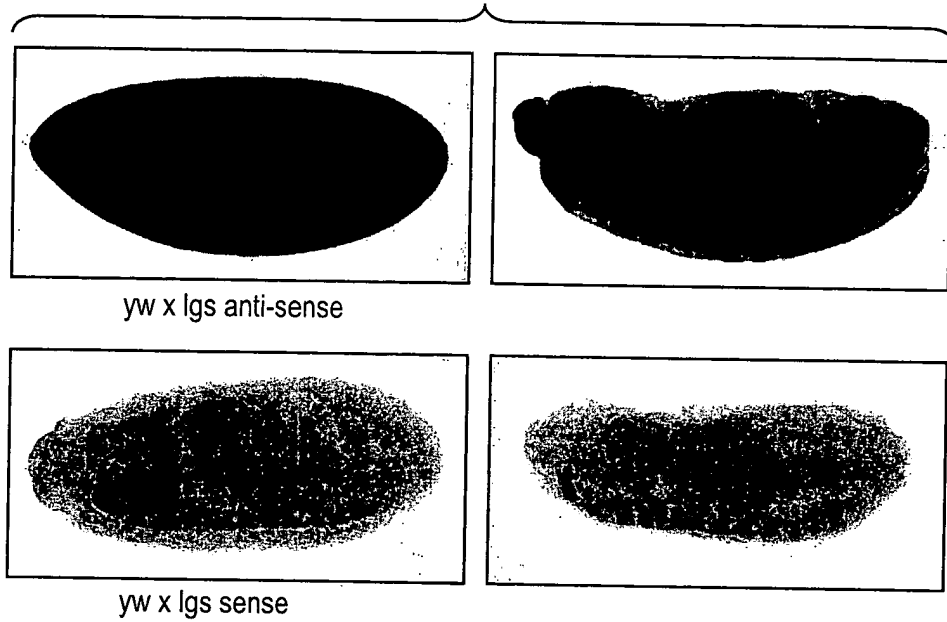


FIG. 3B

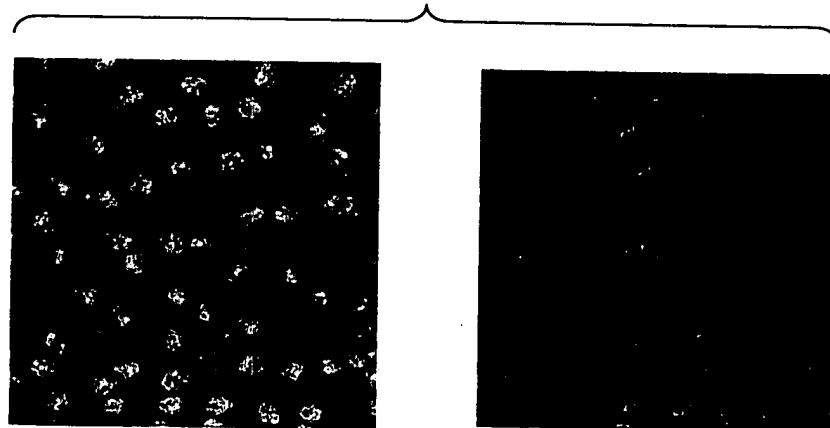


FIG. 4

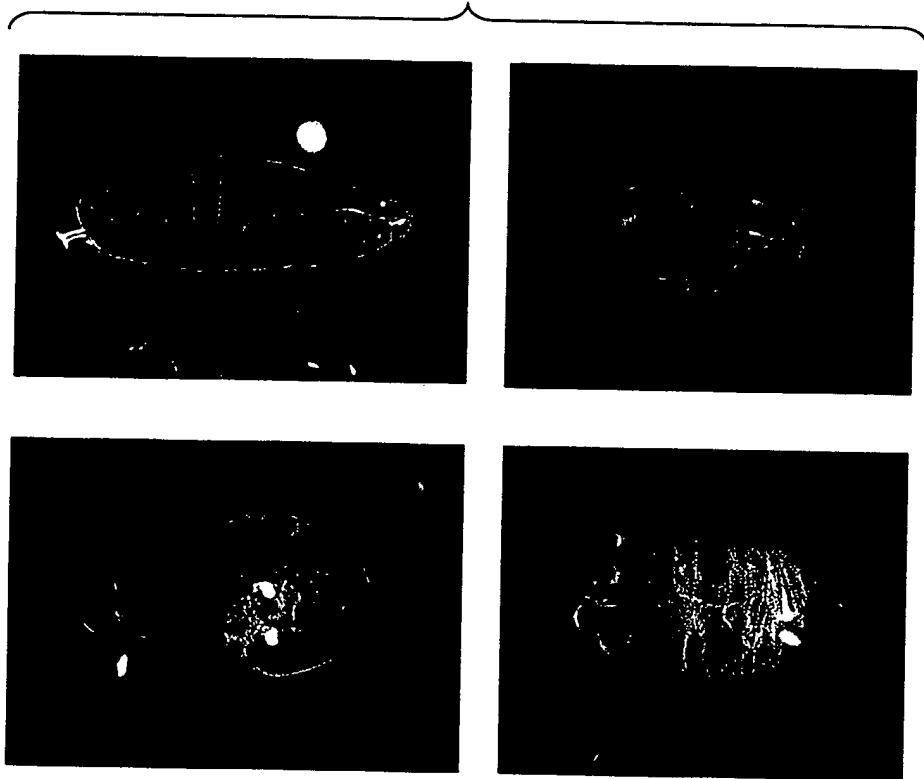


Figure 5A

EGFP-Lgs

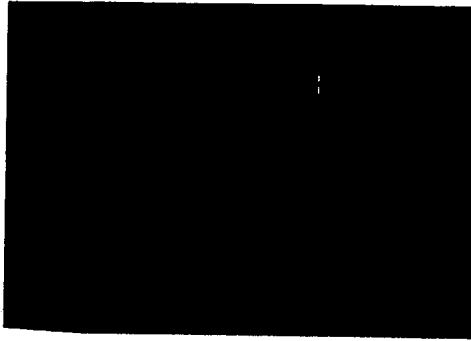


Figure 5B

EGFP-Lgs + pcDNA3-Arm-NLS

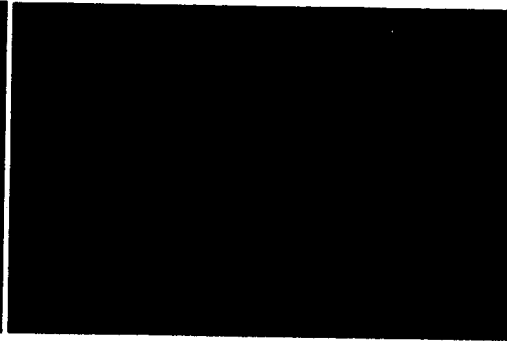


Figure 5A

EGFP-Lgs

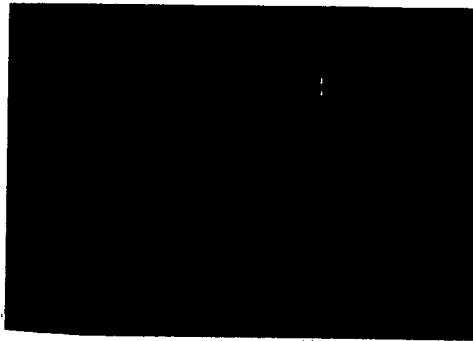


Figure 5B

EGFP-Lgs + pcDNA3-Arm-NLS

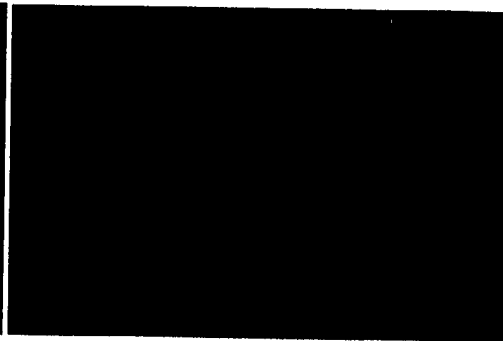


Figure 5A

EGFP-Lgs

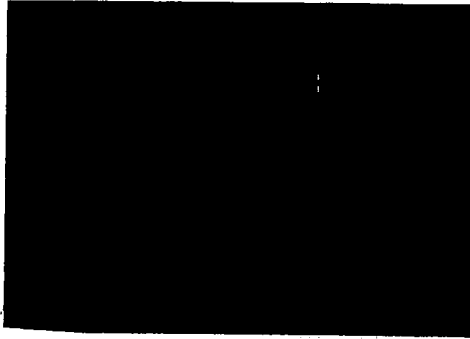


Figure 5B

EGFP-Lgs + pcDNA3-Arm-NLS



Figure 5C

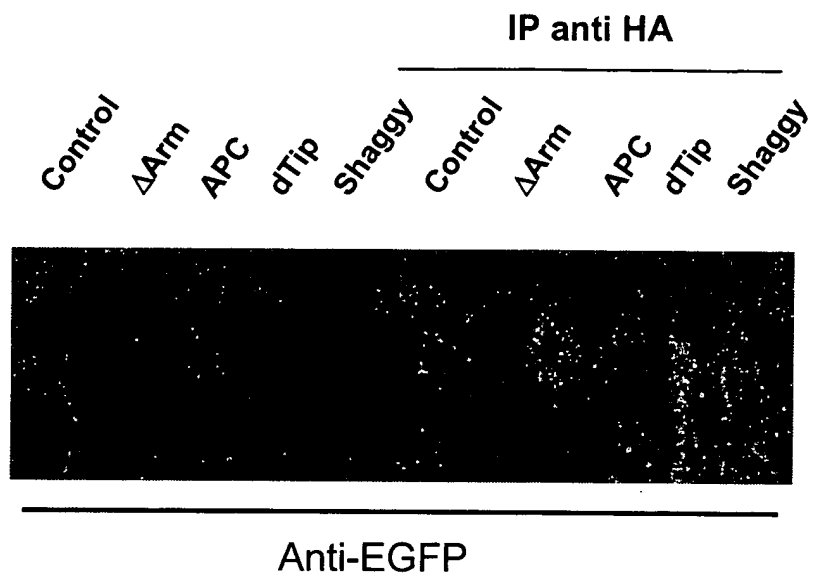


Figure 5D

		BAIT fusions: pLex						
		Lgs 1-1464	BCL9 199-392	BCL9 1-1426	Dco+	Δ ArmC	$\Delta\beta$ -Cat	Pan
PREY fusions: pJG4-5	lgs364-555					+		
	lgs1-385					+		
	lgs1-732					+		
	lgs364-1090					+		
	lgs726-1464					+		
	lgs1-1464				+	+	n.d.	+
	BCL9 199-392					+	n.d.	
	BCL91-1426					+	+	
	Dco+	+						
	DAxin	(+)				+		
	Δ ArmC	+	+	+				+
	β -Cat	+	+	+				
	Pan	+				+		
	pJG4-5	+	+	+		+	+	

+: interaction seen in yeast two-hybrid assay
 -: no interaction seen in yeast two-hybrid assay
 n.d.: not done
 numberings refer to amino acid positions.

Figure 5E

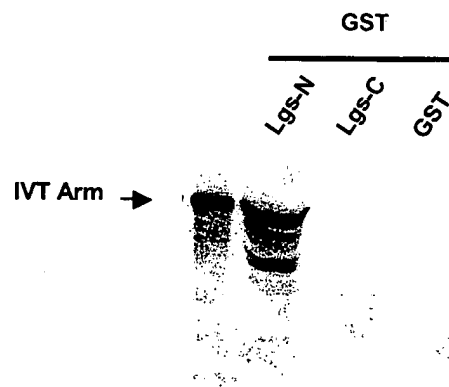


Figure 5F

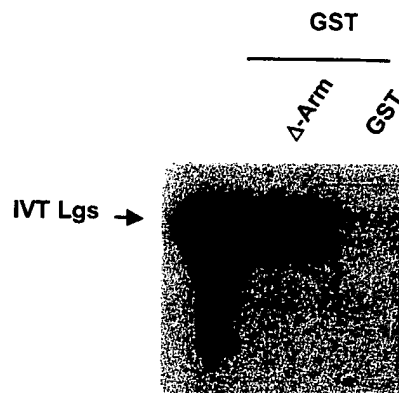


Figure 5G

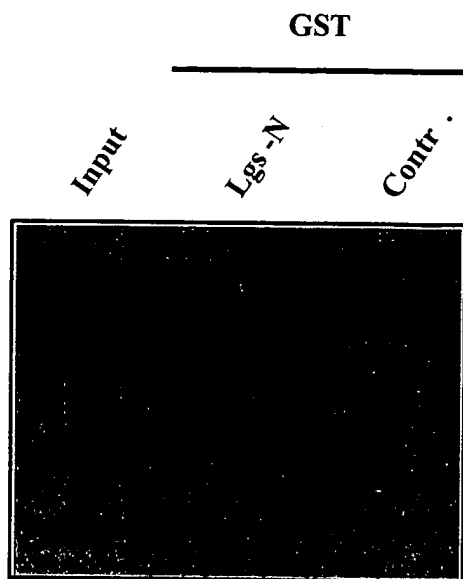


FIG. 6

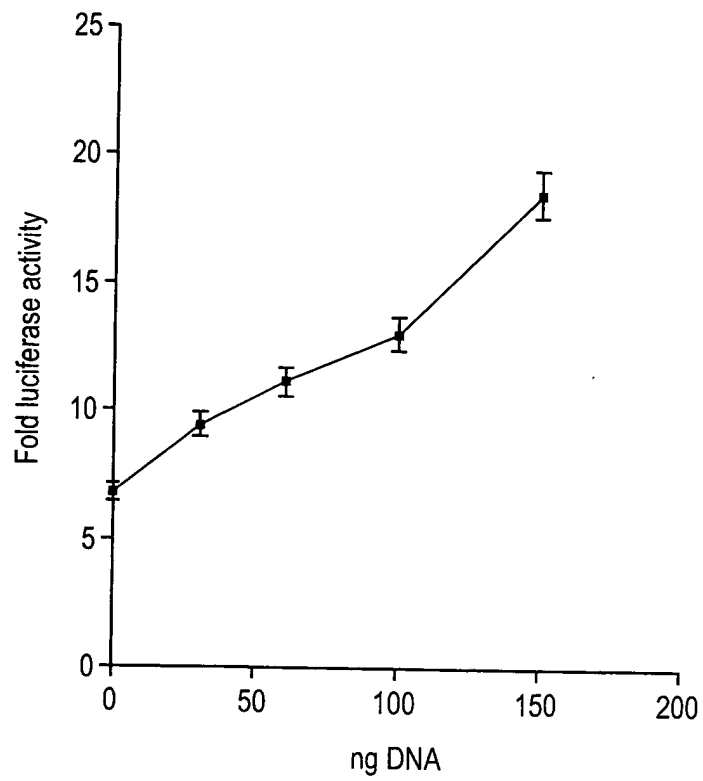


FIG. 7A

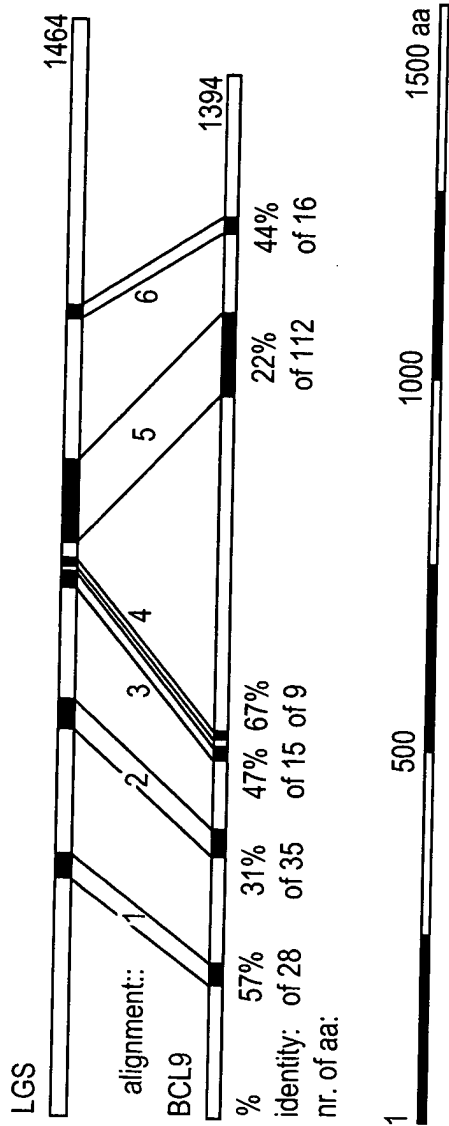


FIG. 7B

Sequence homology domain 1:57.1% identity in 28 aa

	320	330	340
LGS	IFVFSTQLANKGAESVLSGQFQTIIAYH		

BCL9	VYVFSTEMANKAAEAVLKGQVETIVSFH		
	180	190	200

Sequence homology domain 2:31.4% identity in 35 aa

	520	530	540
LGS	ENLTPQQRQHREEQLAKIKKMNQFLFPENENSVGA		

BCL9	DGLSQEQLEHRERSLQTLRDIQRLMFPDEKEFTGA		
	350	360	370 380

Sequence homology domain 3:46.7% identity in 15 aa

	710	720
LGS	QMEWSKIQHQFFEER	
	
BCL9	QIAWLKLQQEFYEEK	
	470	480

Sequence homology domain 4:66.6% identity in 9 aa

	760
LGS	LQGPPPPYH

BCL9	VRGPPPPYQ
	520

Sequence homology domain 5:22.3% identity in 112 aa

	770	780	790	800	810	820
LGS	SASVPIATQSPNPSSPNNLSLPSRPTTAAVMGLPTNSPMDGTGSLSGSVQANTSTVQA					

BCL9	GPPPTASQPASVNI PGSLSSTPYTMPPEPTLSQNPLSIM-MSRMSKFAMPSSTPLYHD					
	970	980	990	1000	1010	1020
	830	840	850	860	870	
LGS	GTTTVLSANKNCFQADTPSPSNQNRSRNTGSSSVLTHNLSSNPSTPLSHLSP					

BCL9	AIKTVASSDDSDPPARSPNLPSMNNMPGMGINTQNPRISGPNPVVPMPTLSP					
	1030	1040	1050	1060	1070	

Sequence homology domain 6:43.8% identity in 16 aa

	1080	
LGS	NPKMCVAGGPNGPPGF	
	
BCL9	DAALCKPGGPGGPDSE	
	1190	1200

Figure 8A

ATGCATTCCAGTAACCCCTAAAGTGAGGAGCTCTCCATCAGGAAACACACA
GAGTAGCCCTAAGTCAAAGCAGGAGGTGATGGTCCGTCCTCCCTACAGTGA
TGTCCCATCTGGAAACCCCCAGCTGGATTCCAAATTCTCCAATCAGGGT
AAACAGGGGGGCTCAGCCAGCCAATCCCAGCCATCCCCCTGTGACTCCAA
GAGTGGGGGCCATACCCCTAAAGCACTCCCTGGCCCAGGTGGGAGCATGG
GGCTGAAGAATGGGGCTGGAAATGGTGCCAAGGGGCAAGGGGAAAAGGGAG
CGAAGTATTTCCGCCGACTCCTTTGATCAGAGAGATCCTGGGACTCCAAA
CGATGACTCTGACATTAAAGAATGTAATTCTGCTGACCACATAAAGTCCC
AGGATTCCCAGCACACACCACACTCGATGACCCCATCAAATGCTACAGCC
CCCAGGTCTTCTACCCCTCCCATGGCCAACTACTGCCACAGAGCCCAC
ACCTGCTCAGAAGACTCCAGCCAAAGTGGTGTACGTGTTTTCTACTGAGA
TGGCCAATAAAGCTGCAGAAGCTGTTTTGAAGGGCCAGGTTGAACTATC
GTCTCTTTCCACATCCAGAACATTTCTAACAACAAGACAGAGAGAAGCAC
AGCGCCTCTGAACACACAGATATCTGCCCTTCGGAATGATCCGAAACCTC
TCCCACAACAGCCCCCAGCTCCGGCCAACCAGGACCAGAATTCTTCCCAG
AATACCAGACTGCAGCCAACTCCACCCATTCCGGCACCAGCACCCAAAGCC
TGCCGCACCCCCACGTCCCCTGGACCGGGAGAGTCCTGGGGTAGAAAACA
AACTGATTCTTCTGTAGGAAGTCCTGCCAGCTCCACTCCACTGCCCCCA
GATGGTACTGGGCCCAACTCAACTCCCAACAATAGGGCAGTGACCCCTGT
CTCCCAGGGGAGCAATAGCTCTTCAGCAGATCCCAAAGCCCTCCGCCTC
CACCAGTGTCCAGTGGCGAGCCCCCACACTGGGAGAGAATCCCGATGGC
CTATCTCAGGAGCAGCTGGAGCACCGGGAGCGCTCCTTACAACTCTCAG
AGATATCCAGCGCATGCTTTTTCTGATGAGAAAGAATTCACAGGAGCAC
AAAGTGGGGGACCGCAGCAGAATCCTGGGGTATTAGATGGGCCTCAGAAA
AAACCAGAAGGGCCAATACAGGCCATGATGGCCCAATCCCAAAGCCTAGG
TAAGGGACCTGGGCCCGGACAGACGTGGGAGCTCCATTTGGCCCTCAAG
GACATAGAGATGTACCCTTTTCTCCAGATGAAATGGTTCCACCTTCTATG
AACTCCAGTCTGGGACCATAGGACCCGACCACCTTGACCATATGACTCC
CGAGCAGATAGCGTGGCTGAAACTGCAGCAGGAGTTTTATGAAGAGAAGA
GGAGGAAGCAGGAACAAGTGGTTGTCCAGCAGTGTTCCTCCAGGACATG
ATGGTCCATCAGCACGGGCCTCGGGGAGTGGTCCGAGGACCCCCCTCC
ATACCAGATGACCCCTAGTGAAGGCTGGGCACCTGGGGGTACAGAGCCAT
TTTCTGATGGTATCAACATGCCACATTCTCTGCCCCGAGGGGCATGGCT
CCCCACCCCAACATGCCAGGGAGCCAGATGCGCCTCCCTGGATTTGCAGG
CATGATAAACTCTGAAATGGAAGGGCCGAATGTCCCAACCCTGCATCTA
GACCAGGTCTTCTGGAGTCAGTTGGCCAGATGATGTGCCAAAAATCCCA
GATGGTTCGAAATTTTCTCCTGGCCAGGGCATTTCAGCGGTCTTGCCG
AGGGGAACGCTTCCCAAACCCCAAGGATTGTCTGAAGAGATGTTTCAGC
AGCAGCTGGCAGAGAAACAGCTGGGTCTCCCCCAGGGATGGCCATGGAA
GGCATCAGGCCCAGCATGGAGATGAACAGGATGATTCCAGGCTCCAGCG
CCACATGGAGCCTGGGAATAACCCCATTTTCCCTCGAATACCAGTTGAGG
GCCCTCTGAGTCCTTCTAGGGGTGACTTTCCAAAAGGAATTCCCCCACAG

Figure 8A (Cont.)

ATGGGCCCTGGTCGGGAACTTGAGTTTGGGATGGTTCCTAGTGGGATGAA
GGGAGATGTCAATCTAAATGTCAACATGGGATCCAACTCTCAGATGATAC
CTCAGAAGATGAGAGAGGCTGGGGCGGGCCCTGAGGAGATGCTGAAATTA
CGCCCAGGTGGCTCAGACATGCTGCCTGCTCAGCAGAAGATGGTGCCACT
GCCATTTGGTGAGCACCCCCAGCAGGAGTATGGCATGGGCCCCAGACCAT
TCCTTCCCATGTCTCAGGGTCCAGGCAGCAACAGTGGCTTGCGGAATCTC
AGAGAACCAATTGGGCCCGACCAGAGGACTAACAGCCGGCTCAGTCATAT
GCCACCACTACCTCTCAACCCTTCCAGTAACCCCAACCAGCCTCAACACAG
CTCCTCCAGTTCAGCGCGGCCTGGGGCGGAAGCCCTTGGATATATCTGTG
GCAGGCAGCCAGGTGCATTCCCCAGGCATTAACCCTCTGAAGTCTCCAC
GATGCACCAAGTCCAGTCACCAATGCTGGGCTCGCCCTCGGGGAACCTCA
AGTCCCCCAGACTCCATCGCAGCTGGCAGGCATGCTGGCGGGCCAGCT
GCTGCTGCTTCCATTAAGTCCCCCCTGTTTTGGGGTCTGCTGCTGCTTC
ACCTGTCCACCTCAAGTCTCCATCACTTCCTGCCCCGTACCTGGATGGA
CCTCTTCTCCAAAACCTCCCCTTCCAGAGTCCTGGGATCCCTCCAAACCAT
AAAGCACCCCTCACCATGGCCTCCCCAGCCATGCTGGGAAATGTAGAGTC
AGGTGGCCCCCACCTCCTACAGCCAGCCAGCCTGCCTCTGTGAATATCC
CTGGAAGTCTTCCCTCTAGTACACCTTATACCATGCCTCCAGAGCCAACC
CTTTCCCAGAACCCACTCTCTATTATGATGTCTCGAATGTCCAAGTTTGC
AATGCCCAGTTCCACCCGTTATACCATGATGCTATCAAGACTGTGGCCA
GCTCAGATGACGACTCCCCTCCAGCTCGTTCTCCCAACTTGCCATCAATG
AATAATATGCCAGGAATGGGCATTAATACACAGAATCCTCGAATTTTCAGG
TCCAAACCCCGTGGTTCCGATGCCAACCCTCAGCCCAATGGGAATGACCC
AGCCACTTTCTCACTCCAATCAGATGCCCTCTCCAAATGCCGTGGGACCC
AACATACCTCCTCATGGGGTCCCAATGGGGCCTGGCTTGATGTACACAA
TCCTATCATGGGGCATGGGTCCCAGGAGCCACCGATGGTACCTCAAGGAC
GGATGGGCTTCCCCCAGGGCTTCCCTCCAGTACAGTCTCCCCACAGCAG
GTTCCATTCCCTCACAATGGCCCCAGTGGGGGGCAGGGCAGCTTCCCAGG
AGGGATGGGTTTCCCAGGAGAAGGCCCCCTTGGCCGCCCCAGCAACCTGC
CCCAAAGTTCAGCAGATGCAGCACTTTGCAAGCCTGGAGGGCCCCGGGGT
CCTGACTCCTTCACTGTCTGGGGAACAGCATGCCTTCGGTGTTTACAGA
CCCAGATCTGCAGGAGGTCATCCGACCTGGAGCCACCGGAATACCTGAGT
TTGATCTATCCCGCATTATTCCATCTGAGAAGCCCAGCCAGACGCTGCAA
TATTTCCCTCGAGGGGAAGTTCCAGGCCGTAAACAGCCCCAGGGTCTGG
ACCTGGGTTTTTACACATGCAGGGGATGATGGGCGAACAAGCCCCAGAA
TGGGACTAGCATTACCTGGCATGGGAGGTCCAGGGCCAGTGGGAACTCCG
GACATCCCTCTTGGTACAGCTCCATCCATGCCAGGCCACAACCCCATGAG
ACCACCAGCCTTTCTCCAACAAGGCATGATGGGACCTCACCATCGGATGA
TGTCACCAGCACAATCTACAATGCCCGGCCAGCCACCCTGATGAGCAAT
CCAGCTGCTGCCGTGGGCATGATTCTGGCAAGGATCGGGGGCCTGCCCG
GCTCTACACCCACCCTGGGCCTGTGGGCTCTCCAGGCATGATGATGTCCA
TGCAGGGCATGATGGGACCCCAACAGAACATCATGATCCCCCACAGATG
AGGCCCGGGGCATGGCTGCTGACGTGGGCATGGGTGGATTAGCCAAGG
ACCTGGCAACCCAGGAAACATGATGTTTTAA

Figure 8B

MHSSNPKVRSSPSGNTQSSPKSKQEVMPVPPTVMSPSGNPQLDSKFSNQG
KQGGASASQSPSPCDSKSGGHTPKALPGPGGSMGLKNGAGNGAKGKGKRE
RSISADSFQDRDPGTPNDDSDIKECNSADHIKSQDSQHTPHSMTPSNATA
PRSSTPSHGQTTATEPTPAQKTPAKVVYVFSTEMANKAAEAVLKQVETI
VSFHIQNISNNKTERSTAPLNTQISALRNDPKPLPQQPPAPANQDQNSSQ
NTRLQPTPIIPAPAPKPAAPPRPLDRESPGVENKLIPSVGSPASSTPLPP
DGTGPNSTPNNRAVTPVSQGSNSSSADPKAPPPPPVSSGEPPTLGENPDG
LSQEQLEHRERSLQTLRDIQRMLFPDEKEFTGAQSGGPQQNPGVLDGPQK
KPEGPIQAMMAQSQSLGKGPGPRTDVGAPFGPQGHHRDVPFSPDEMVPSPM
NSQSGTIGPDHLDHMTPEQIAWLKLQQEFYEEKRRKQEQVVVQQCSLQDM
MVHQHGPRGVVRGPPPPYQMTPEGWAPGGTEPFSDGINMPHSLPPRGMA
PHPNMPGSQMRLPGFAGMINSEMEGPNVNPASRPGLSGVSWPDDVPKIP
DGRNFPFGQGFSGPGRGERFPNPQGLSEEMFQQQLAEKQLGLPPGMAME
GIRPSMEMNRMIPGSQRHMEPGNNPIFPRIPEGLSPSRGDFPKGIPPQ
MGPGRELEFGMVPSPGMKGDVNLNVNMGSSNSQMIPQKMREAGAGPEEMLKL
RPGGSDMLPAQQKMVPLPFGHEHPQQEYGMGPRPFLPMSQGPSSNSGLRNL
REPIGPDQRTNSRLSHMPPLPLNPSSNPTSLNTAPPVQRGLGRKPLDISV
AGSQVHSPGINPLKSPTMHQVQSPMLGSPSGNLKSPQTPSQLAGMLAGPA
AAASIKSPPVLGSAAASPVHLKSPSLPAPSPGWTSSPKPPLQSPGIPPNH
KAPLTMASPAMLGNVESGGPPPPTASQPASVNIPGSLPSSTPYTMPPEPT
LSQNPLSIMMSRMSKFAMPSSTPLYHDAIKTVASSDDDSPPARSPNLPSM
NNMPGMGINTQNPRISGPNPVVPMPTLSPMGMTQPLSHSNQMPSPNAVGP
NIPPHGVPMGPGLMSHNPIMGHGSQEPPMVPQGRMGFPQGFPVQSPQQ
VPFPHNGPSGGQGSFPGGMGFPGEGLGRPSNLPQSSADAALCKPGGPGG
PDSFTVLGNSMPSVFTDPLQEVIRPGATGIPEFDLSRIIPSEKPSQTLQ
YFPRGEVPGRKQPQGGPGGFSHMQGMGEQAPRMGLALPGMGGPGPVGTP
DIPLGTA SMPGHNPMPAFLQQGMMGPHHRMMSPAQSTMPGQPTLMSN
PAAVGMIPGKDRGPAGLYTHPGVPVSGPMMMSMQGMMGPQQNIMIPPQM
RPRGMAADVGMGGFSQGGPNPGNMMF*

FIG. 9

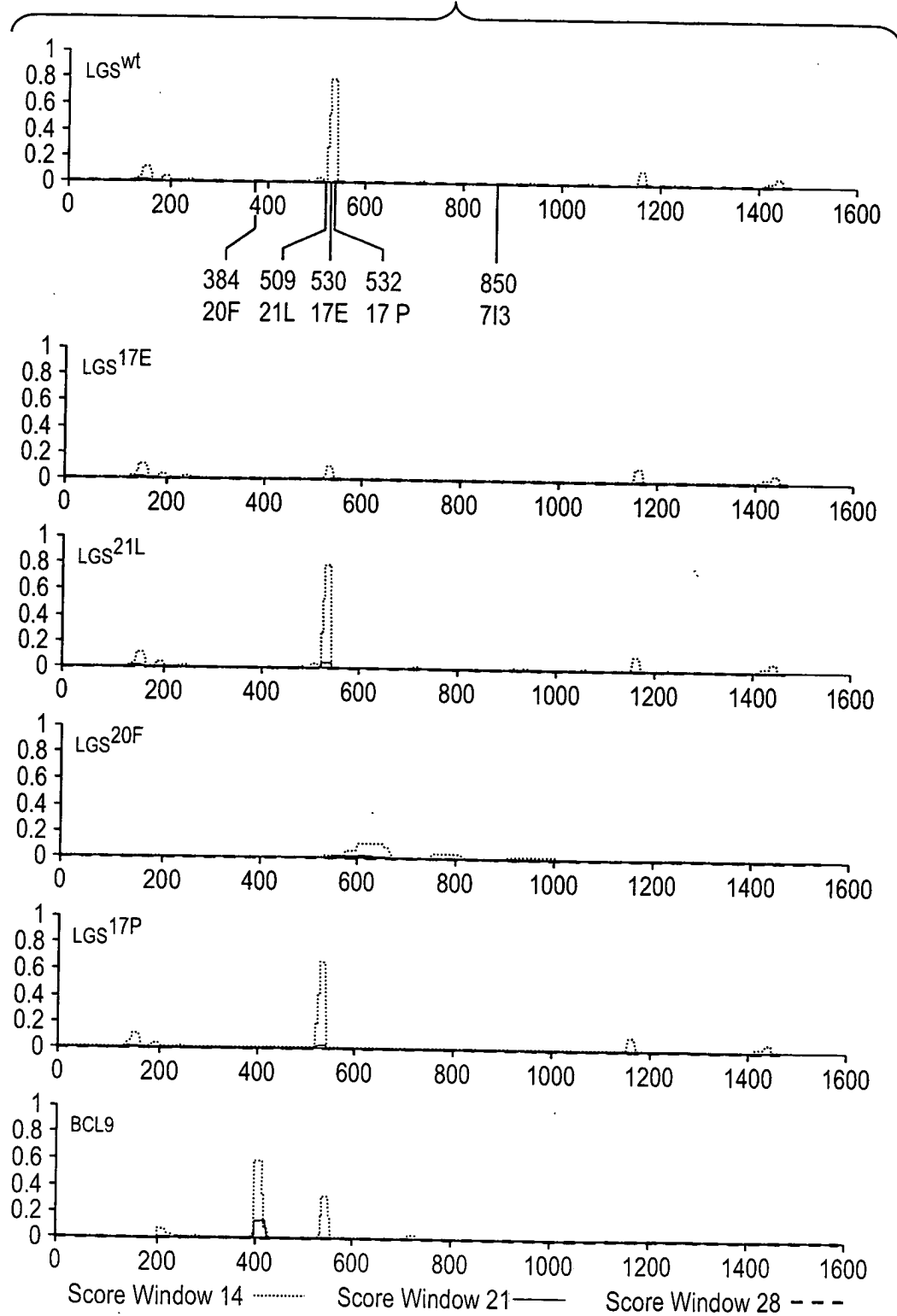


Figure 10A

ATGGCCTGCTTCCCATCCCCTGCTGCCATCTCCTGCACCCTTAGGGCACAGTGGGCATCT
CGGGAGCTGCTCAGCGGACAGACTAGGGTTACCCCCACCCAGGAGGAGAGAAGCTCCAG
GGAGCCCGCCGCTGTCCCCCGGGTCATTGCCCCCTGCCCCAGCCAAGCCAATGCACCCA
GAAATAAATTGACCAATCATGGCAAGACAGGGAATGGCGGGGCCCAATCTCAGCACCAG
AATGTGAACCAAGGACCCACCTGCAACGTGGGCTCGAAGGGCGTGGGGGCGGGGAACCAT
GGGGCCAAGGCCAACCAGATCTCGCCTAGCAACTCAAGTCTGAAGAACCCCCAGGCAGGG
GTGCCCCCTTTTACGCTCGCTCAAGGGCAAGGTGAAGAGGGACCGAGTGTGTCTGTGGAC
TCTGGAGAGCAGCGAGAGGCTGGGACCCCATCCCTGGATTTCAGAGGCCAAAGAGGTGGCG
CCGCGGAGTAAGCGGCGCTGTGTGCTGGAGCGGAAGCAGCCGTACAGTGGGGACGAATGG
TGCTCTGGACCGGACAGTGAGGAGGACGACAAGCCCATTTGGGGCCACCCACAAAGCTGCT
TTCAAAGAAGACGGCTTTCAGGACAAGGCATCACACTTCTTCTCCAGCACGTACAGTCCCT
GAAACCTCCAGGAGGAAGCTGCCCCAAGCCCCGAAGGCTTCCCTTCTTGGGGCAGCAGGGC
CGAGTCATTTGGAACCTCTCTCGGAGGAGCTCCGTGATCAAGGTGCAGATGCGGCAGGT
GGCCCGCCCTCAATCATGTCTCCAATCGCGACGGTGAATGCGAGTGGCTTGTCCAAAGAG
CAGCTGGAGCATCGGGAACGGTCCCTCCAGACGCTGCGAGACATTGAGCGACTGCTGCTC
CGCAGCGGAGAGACTGAGCCCTTCTCAAGGGGGCCCCCAGGAGGAGCGCGGGCTGAAG
AAATATGAGGAACCTTTCAGTCCATGATTTTACAGACACAGAGCCTAGGGGGCCCCCG
CTGGAGCATGAAGTGCTGGGCACCCCCCGGGTGGGGACATGGGGCAGCAGATGAACATG
ATGATACAGAGGCTGGGCCAGGACAGCCTCACGCCTGAGCAGGTGGCTTGGCGCAAGCTG
CAGGAGGAGTACTACGAAGAGAAACGGCGGAAAGAGGAACAGATTGGGCTGCATGGGAGC
CGTCTCTGCGAGGACATGATGGGCATGGGGGGCATGATGGTGAGGGGGCCCCCGCTCCT
TACCACAGCAAGCCTGGGGATCAGTGGCCACCTGGAATGGGTGCGCAGCTGCGGGGGCCC
ATGGATGTTCAAGATCCCATGCAGCTCCGGGGCGGACCTCCCTTTCTTGGGGCCCCGTTTC
CCAGGCAACCAGATACAACGGGTACCTGGGTTTGGGGGCATGCAGAGTATGCCCATGGAG
GTGCCCATGAATGCCATGCAGAGGCCCTGAGACCAGGCATGGGCTGGACCGAAGACTTG
CCCCCTATGGGGGGACCCAGCAATTTTGGCCAGAACACCATGCCCTACCCAGGTGGGCAG
GGTGAGGCGGAGCGATTTCATGACTCCCCGGGTCCGTGAGGAGCTGCTGCGGCACCAGCTG
CTGGAGAAGCGGTCGATGGGCATGCAGCGCCCCCTGGGCATGGCAGGCAGTGGCATGGGA
CAGAGCATGGAGATGGAGCGGATGATGCAGGCGCACCGACAGATGGATCCTGCCATGTTT
CCCGGGCAGATGGCTGGTGAGGGCTGGCGGGCACTCCCATGGGCATGGAGTTTGGT
GGAGGCCGGGGCTCCTGAGCCCTCCCATGGGGCAGTCTGGGCTGAGGGAGGTGGACCCA
CCCATGGGGCCAGGCAACCTCAACATGAACATGAATGTCAACATGAACATGAACATGAAC
CTGAACGTGCAGATGACCCCGCAGCAGCAGATGCTGATGTGCGAGAAGATGCGGGGCCCT
GGGACTTGTATGGGGCCCCAGGGCCTCAGTCCCTGAGGAGATGGCCCGGGTTCGGGGCCAG
AACAGCAGTGGCATGGTGCCCTTGCCCTTCTGCCAACC CGCCAGGACCTCTCAAGTCGCCC
CAGGTCCCTCGGCTCCTCCCTCAGTGTCCGTTACCCACTGGCTCGCCAGCAGGCTCAAG
TCTCCTTCCATGGCGGTGCCTTCTCCAGGCTGGGTGCTTACCCCAAGACGGCCATGCC
AGCCCGGGGTCTCCAGAACAAGCAGCCGCTCTCAACATGAACCTTCCACCACCCCTG
AGCAACATGGAACAGGACCCACACCTTCCCAAGAACCCCTGTCACTGATGATGACCCAG
ATGTCCAAGTACGCCATGCCAGCTCCACCCCGCTCTACCACAATGCCATCAAGACCATC
GCCACCTCAGACGACGAGCTGCTGCCCCGACCGGCCCTGCTGCCCCCCCCACCACCAGC
CAGGGCTCCGGGGCAGGTGGCCCCGACTCCCTGAATGCCCCCTGTGGCCAGTGGCCAGC
TCCTCCCAGATGATGCCCTTCCCCCTCGGCTGCAGCAGCCCCATGGTGCCATGGCCCCC
ACTGGGGGTGGGGGCGGGGGGCTGGCCTGCAGCAGCACTACCCGTGAGGCATGGCCCTG
CCTCCCGAGGACCTGCCCAACCAGCCGCCAGGCCCATGCTCCCCAGCAGCAGCTGATG
GCCAAAGCCATGGCTGGGCGCATGGGCGACGCATACCCACCGGGTGTGCTCCCTGGGGTG
GCATCAGTGCTGAACGACCCCGAGCTGAGCGAGGTGATCCGGCCCCACCCCAACGGGGATC
CCCGAGTTGCACTTGTGAGGATCATCCCTCTGAGAAGCCAAGCAGCAGCCCTCCAGTAC
TTCCCAAGAGCGAGAACCAGCCCCCAAGGCTCAGCCCCCTAATCTGCATCTCATGAAC
CTGCAAGAACATGATGGCGGAGCAGACTCCCTCTCGGCCCTCCCAACCTCCCAGGCCAGCAG
GGCGATCGGCCGCTGGTGGTGGTGATACCGGTACCCGGGCTATGGCGCCGGCGCAGCGC
TGCCCTCTGTGCGCGCAGACCTTCTTCTGTGGTTCGCGGGCACGTTTACAGCCGAAGCAC
CAGCGGCAGCTGAAGGAGGCTTGGAGAGGCTCCTGCCCCAGGTGGAGGCGGCCCGCAAG
GCCATCCGCGCCGCTCAGGTGGAGCGCTATGTGCCCGAACACGAGCGATGCTGCTGGTGC
CTGTGCTGCGGCTGTGAGGTGCGGGAACACCTGAGCCATGGAACCTGACGGTGCTGTAC

Figure 10A (Cont.)

GGGGGGCTGCTGGAGCATCTGGCCAGCCCAGAGCACAAAGAAAGCAACCAACAAATTC TGG
TGGGAGAACAAAGCTGAGGTCCAGATGAAAGAGAAGTTTCTGGTCACTCCCCAGGATTAT
GCGCGATTCAAGAAATCCATGGTGAAAGGTTTGGATTCCCTATGAAGAAAAGGAGGATAAA
GTGATCAAGGAGATGGCAGCTCAGATCCGTGAGGTGGAGCAGAGCCGACAGGAGGTGGTT
CGGTCTGTCTTAGAGACAGGTCCCCCAAGATACGCCCCACAGTCCGGTCCCCCGCCGTC
CTCTCCCGGCGCACGCTCAAGTCCGGTGCCTTCCCCCGCAGACCCCCGAGGCGCACCCCT
CAAGCTCGGTGCCTCTGCGCCCCCGCAGGGGCGCCCTCAAGCCTGAGCCCCCGGGCGC
ACCCTCAAGCTCGGTGTACCCCCCATACCAACCGCAAGGCGCGCCCTCATGCCGCGAAG
ACTTCGCCCCGCCCCAAGGTGCACCCGTCAAGCCCCGAATAAAACCCAGTCACTCCAACCTT
GCAGGCAAAGCTAGAAAAACTGCGCTGCATTTGCAAACAAAAGCTCTTGTTGGCGATGAC
GATACTGTTTGGGTGTGAAACTGTCAATTGCTAACTACGATCTGTGA

Figure 10B

FKEDGFQDKASHFFSSTYSPETSRRKLPQAPKASFLGQQGRVIWKPLSEE
LRDQGADAAGGPASIMSPIATVNASGLSKEQLEHRERSLQTLRDIERLLL
RSGETEPFLKGAPRRSGGLKKYEEPLQSMISQTQSLGGPPLEHEVPGHPP
GGDMGQQMNMIMIQLRGQDSLTPQVAWRKLQEEYYEEKRRKEEQIGLHGS
RPLQDMMGMGGMMVRGPPPPYHSKPGDQWPPGMGAQLRGPMQVQDPMQLR
GGPPFPGRFRPGNQIRVPGFGGMQSMPEVPMNAMQRPVRPGMGWTEDL
PPMGGPSNFAQNTMPYPGGQGEAERFMTPRVREELLRHQLLEKRSMGMQR
PLMAGSGMGQSMEMERMMQAHRQMDPAMFPGQMAGGEGLAGTPMGMEFG
GGRGLLSPPMGQSGLEVDPPMGPGNLMNMNVNMNMNMNLNVQMT PQQQ
MLMSQKMRGPGDLMGPQGLSPEEMARVRAQNSSGMVPLPSANPPGPLKSP
QVLGSSLSVRSPTGSPSRLKSPSMAVPSPGWVASPKTAMPSPGVSQNKQP
PLNMNSSTTLNMEQDPTPSQNPLSLMMTQMSKYAMPSSTPLYHNAIKTI
ATSDDELLPDRPLLPPPPPPQGSGPGGPDNLNAPCGVPVSSSQMMPFPPR
LQPHGAMAPTGGGGGGPGLQQHYPSGMALPPEDLPNQPPGPMPPQQHLM
GKAMAGRMGDAYPPGVLPVASVLNDPELSEVIRPTPTGIPEFDLSRIIP
SEKPSSTLQYFPKSENQPPKAQPPNLHLMNLQNMMAEQTPSRPPNLPQQQ
GDRPLVVVIPGTRAMAPAQRCLCRQTFFCGRGHVYSRKHQRQLKEALER
LLPQVEAARKAIRAAQVERYVPEHERCCWCLCCGCEVREHLSHGNLTVLY
GGLLEHLASPEHKKATNKFWWENKAQVQMKEKFLVTPQDYARFKKSMVKG
LDSYEEKEDKVIKEMAAQIREVEQSRQEVVRSVLETGPPRYALTVRSPAV
LSRRTLKSGAFPPQTPEAHPQARCLCAPRRGALKPEPPGRTLKLGVPHT
TRKARPHAAKTSPRPRCTRQAPNKTQSLQLAGKARKTALHLQTKALVGDD
DTVLGVKLSIANYDL

FIG. 11A



FIG. 11B



FIG. 12A

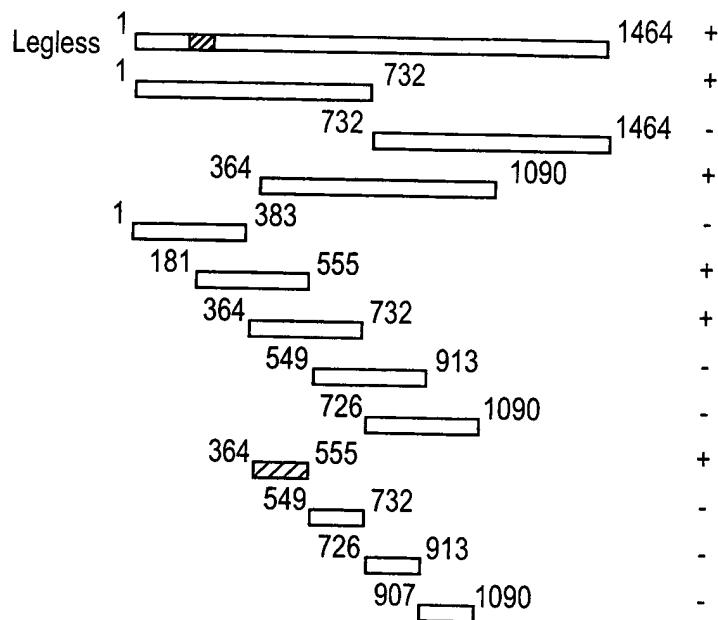


FIG. 12B

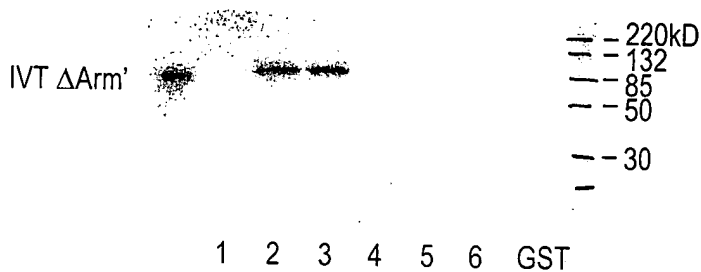
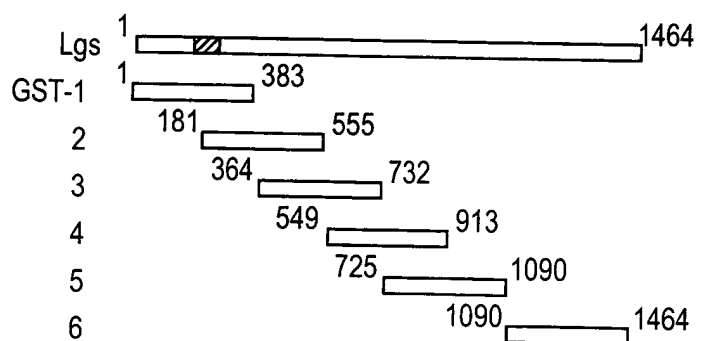


FIG. 12C

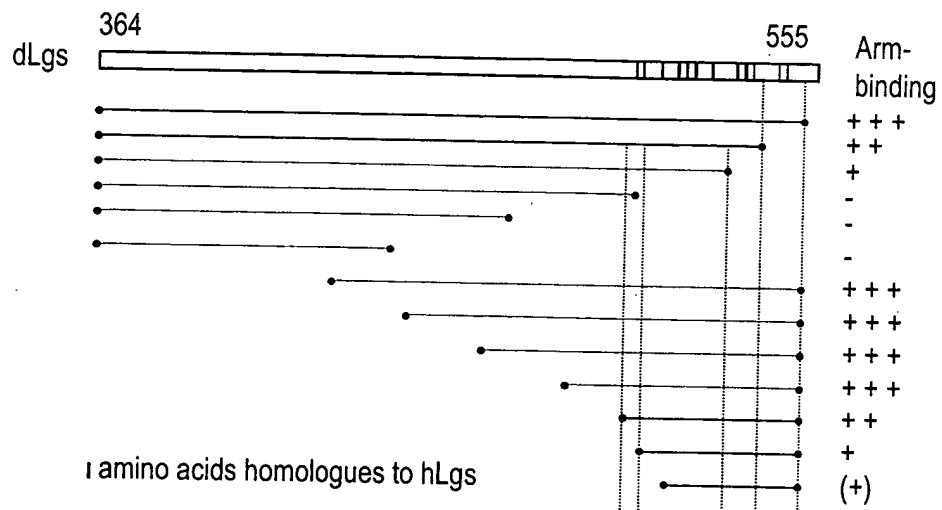


FIG. 12D

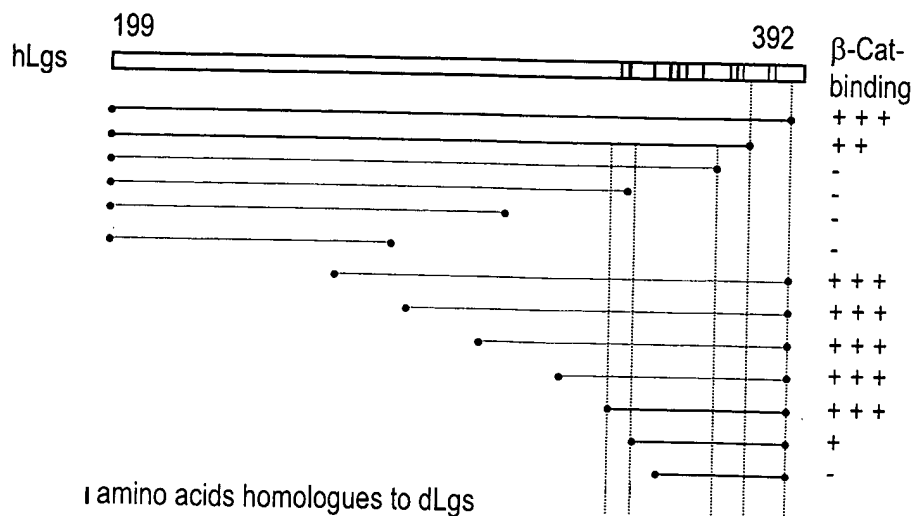


FIG. 12E


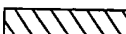
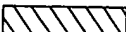


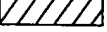
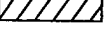
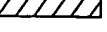
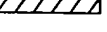
		Invitro interaction
N	 1 2 3 4 5 6 7 8 9 10 11 12 13  C	++
	1 2 3 4 5 6 7 8 9 10 11 12 13  C	++
	 C	-
N	 1 2 3 4 5 6 7 8 9 10 11 12 13	++
N	 1 2 3 4 5 6 7 8	+++
N	 1 2 3 4 5 6	+++
N	 1 2 3 4	++
N	 1 2	-
	1 2 3 4 5 6 7 8 9 10 11 12 13	++
	1 2 3 4 5 6 7 8	+++
	1 2 3 4 5 6	+++
	1 2 3 4	++
	1 2	-
	3 4 5 6 7 8	(+)
	5 6 7 8	(-)
	7 8 9 10 11 12 13	(-)
	9 10 11 12 13	(-)

FIG. 13A

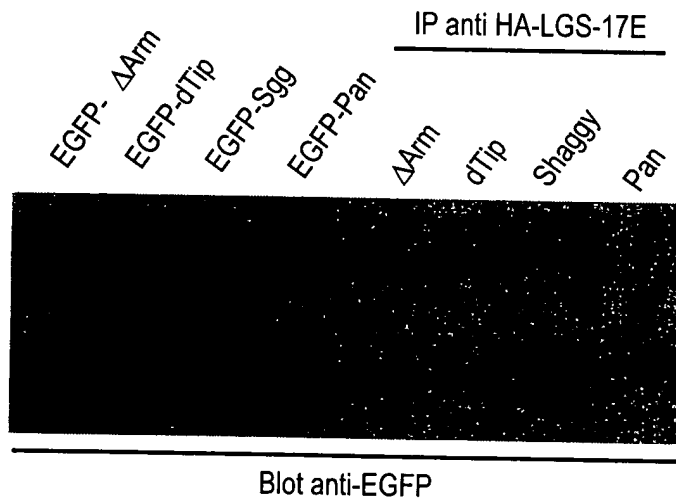


FIG. 13B

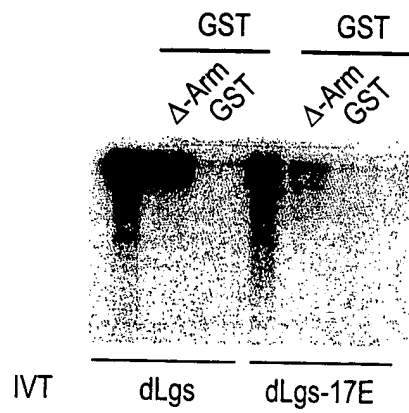


FIG. 13C

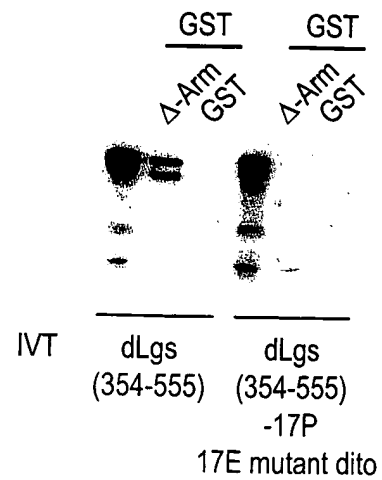


FIG. 13D

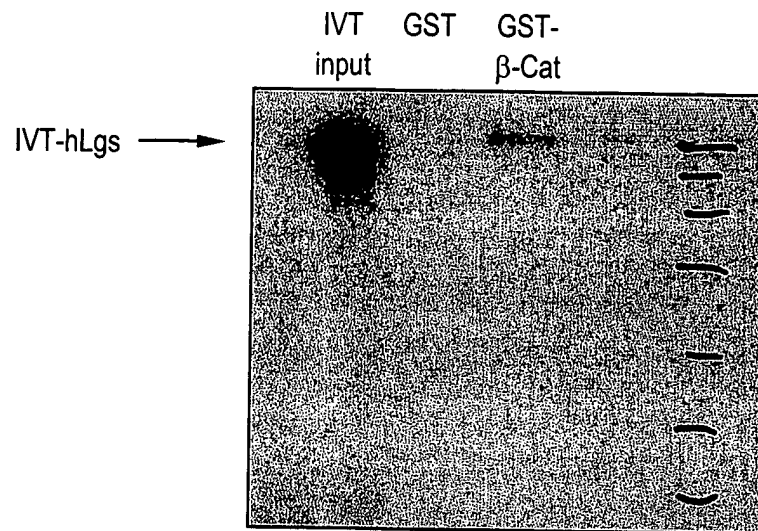


FIG. 13E

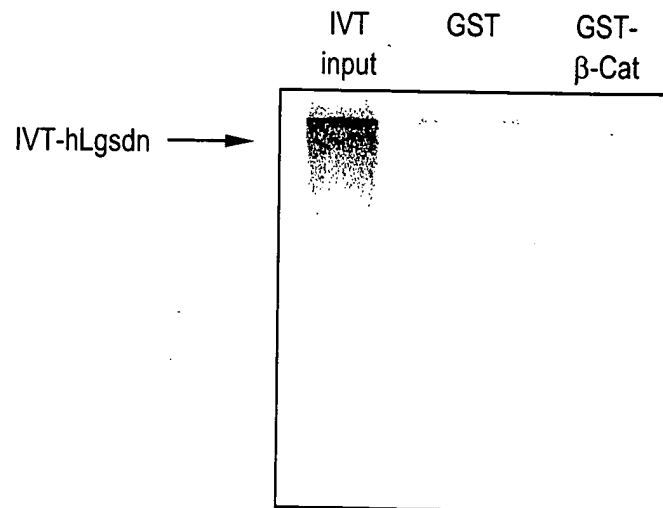


FIG. 14A

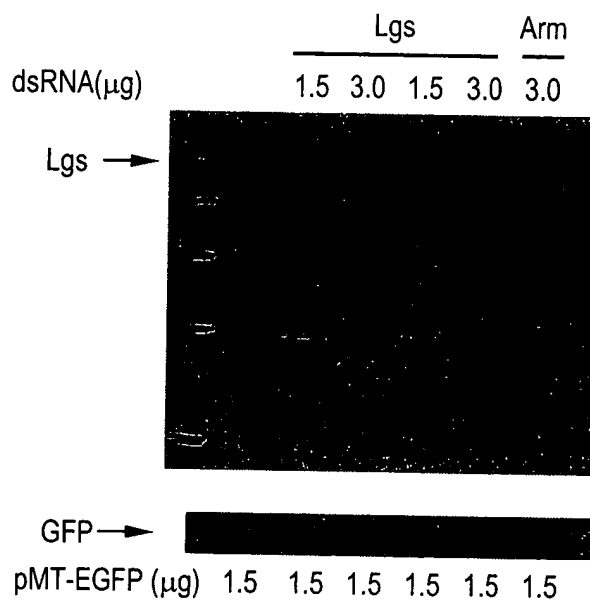


FIG. 14B

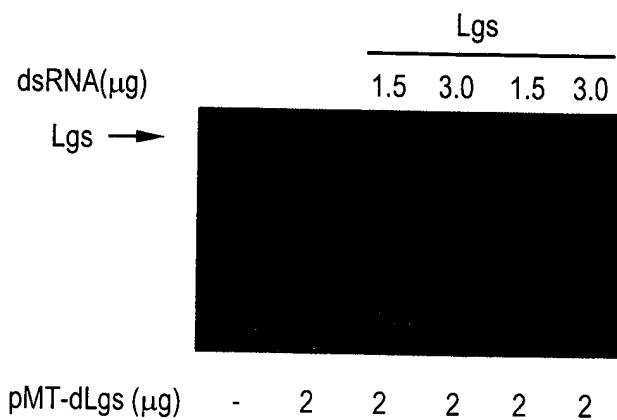


FIG. 15A

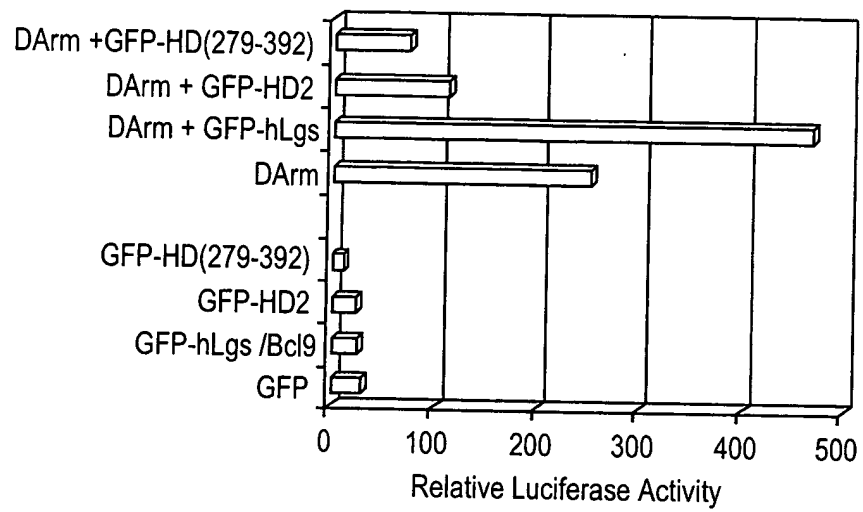


FIG. 15B

